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<110> Roberts, Shannon
Sherman, Amir
Trueheart, Joshua
Milne, G. Todd

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<400> 38
cacagcggcc gcttcattgt ttgcctccct gctg 34

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<400> 40
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20 25 30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
35 40 45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
50 55 60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65 70 75 80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
85 90 95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
100 105 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
115 120 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
130 135 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145 150 155 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
165 170 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
180 185 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
195 200 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
210 215 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225 230 235 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys Arg Gln Gly Thr
245 250 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
260 265 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
275 280 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
290 295 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305 310 315 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
325 330 335
Gly Glu Leu Phe Pro Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
340 345 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu

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        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
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<210> 42
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<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 42

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Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Trp Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Leu Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
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Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Gly Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
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<210> 43
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
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<400> 43

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 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Val Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Ile Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
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145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
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<210> 44
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 44

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            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
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Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Gly Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
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<210> 45
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<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 45

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            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
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```
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
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<210> 46
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 46

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            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Tyr Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Lys Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Ala Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
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```
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
```

<210> 47
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 47

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
```

```
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Ser Ile Pro Pro
465
```

<210> 48
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 48

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
```

```
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Ser Ile Pro Pro
465
```

<210> 49
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 49

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
```

```
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Ser Ile Pro Pro
465

<210> 50
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 50
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
```

```
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Ser Ile Pro Pro
465

<210> 51
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 51
Met Ala Ala Asp Gln Gly Ile Phe Met Asn Ser Val Thr Leu Ser Ala
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Ser Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Lys Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
```

225 230 235 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
245 250 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
260 265 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
275 280 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
290 295 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305 310 315 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
325 330 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
340 345 350
Ala Cys Thr Thr Leu His Val Gly Val Glu Leu Leu Arg Glu Asn Glu
355 360 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
370 375 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385 390 395 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
405 410 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
420 425 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
435 440 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
450 455 460
Asn Asn Ile Pro Pro
465

<210> 52
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 52
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
1 5 10 15
Val Glu Gly Ser His Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
20 25 30
Arg Ala Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
35 40 45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
50 55 60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg His
65 70 75 80
Ser Arg Ala Ser Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
85 90 95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
100 105 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
115 120 125

```
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Asp Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val Asp Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Thr Val Leu Arg Arg Ser Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Ser
465

<210> 53
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 53
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
```

```
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Ile Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
```

<210> 54
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 54

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Ile Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Asp Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asn Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Ser Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Ile Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
```

```
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys Tyr Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
```

<210> 55
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 55

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Val Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
```

```
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Leu Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro Cys
465                 470

<210> 56
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 56
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Ser Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Arg Asp Gly Gly Phe Ser Ser Gln
145                 150                 155                 160
Leu Lys Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
```

```
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Leu Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Asn Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
```

<210> 57
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 57

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Ile Ser Pro
 1               5                  10                  15
Val Val Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
```

```
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Cys Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Gly Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Leu Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Ser Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Ser
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
```

<210> 58
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 58

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Arg Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Tyr Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Thr Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
```

```
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
```

<210> 59
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 59

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Ile Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Gln Val Pro Ser Gln Ser Leu Ser Leu Asp Ile Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
```

305 310 315 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
325 330 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
340 345 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
355 360 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
370 375 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385 390 395 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
405 410 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
420 425 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
435 440 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
450 455 460
Asn Asn Ile Pro Pro
465

<210> 60
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 60
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
1 5 10 15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
20 25 30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
35 40 45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
50 55 60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65 70 75 80
Ser Arg Ala Ala Asn Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
85 90 95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
100 105 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
115 120 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Phe Asp
130 135 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145 150 155 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
165 170 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
180 185 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
195 200 205

```
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Ile Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Ile Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Tyr Ile Ser
    370                 375                 380
Lys Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
```

<210> 61
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 61

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Ile Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Arg Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Arg Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
```

```
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Cys Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Tyr Glu
        355                 360                 365
Ile Thr Leu Gly Ile His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
```

<210> 62
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 62

```
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Arg Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Ile Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Leu Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Asp Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Leu Gly Glu Asp Ile Val Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Ser Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
```

```
    450                 455                 460
Asn Asn Ile Pro Pro
465

<210> 63
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 63
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Asn Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Ile Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Ile Asp Glu Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Ile Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Ala Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
```

```
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
```

<210> 64
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 64

```
Met Ala Ala Glu Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Arg Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Ile Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Glu Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Lys Ala Ile Asp
    130                 135                 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Thr Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
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                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asp Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Arg His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Ile Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Arg Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Thr Phe Gln Glu Ala Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
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<210> 65
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 65

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Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1               5                  10                  15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
            20                  25                  30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35                  40                  45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                  55                  60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65                  70                  75                  80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85                  90                  95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
            100                 105                 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
        115                 120                 125
Ser Tyr Asn Trp Leu Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                 135                 140
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Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                 150                 155                 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                165                 170                 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
            180                 185                 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
        195                 200                 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
    210                 215                 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                 230                 235                 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                245                 250                 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
            260                 265                 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
        275                 280                 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
    290                 295                 300
Ser Arg Ser Gln Ser Pro Ser Gly Asp Asp Thr Ser Ser Ser Ser Gly
305                 310                 315                 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                325                 330                 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
            340                 345                 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
        355                 360                 365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                 375                 380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                 390                 395                 400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                405                 410                 415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Gly Lys Ser Ala
            420                 425                 430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
        435                 440                 445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                 455                 460
Asn Asn Ile Pro Pro
465
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<210> 66
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 66
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300

ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcagtttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccgtc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
ccctatgttg acccccctgac acacgcccta ttctcggctt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaat 1200
tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 67
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 67
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
tggcaatttc ttgatccacc ggacagctac gactggttgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagagtgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacggcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
tcctatgttg acccccctgac acacgcccta ttctcggctt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
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tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 68
<211> 1410
<212> DNA

<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 68
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgccaa 240
tccagggtag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggatctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
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ccactggaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
tcctatgttg acccccctgac acacgcccta ttctcggctt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaat 1200
tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 69
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 69
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttgg aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020

tcctatgttg acccccctgac acacgcccta ttctcggctt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaat 1200
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agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 70
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 70
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
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gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaat 1200
tccgcaagat gcgaggagca gccgactact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 71
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 71
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360

cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatatg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaaa gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
gccgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
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cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
tcctatgttg acccccctgac acacgcccta ttctcggctt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaat 1200
tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 72
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 72
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcgcact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
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cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
tcctatgttg acccccctgac acacgcccta ttctcggctt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaat 1200
tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacagtat tcctccatga 1410

<210> 73
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 73
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gtggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
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gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
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tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 74
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 74
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ttctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccactagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaacgt gcggattttg 840
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cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
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gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
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tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 75
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 75
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
aaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
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gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccca gggcattgca 1140
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 76
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 76
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cgcaccagtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
aaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420

gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacagttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctatcgcaa attaggcgga cccagaacag ccatatgagc 900
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 77
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 77
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cacaccggtg gaacattacc ccgccgtgca ttccgacgcg cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccat 240
tccagggcat cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
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ctcagagacc tcaacaatat tccttcatga 1410

<210> 78
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 78
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cgcaccggtg gaacattacc ccgccgtgca ctccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
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gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
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ctcagagacc tcaacaatat tcctccatga 1410

<210> 79
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 79
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cgcaccggtg gaacattacc ccgccgtgca ctccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat atcctcgcct 300
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gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
cctaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
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gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcaaccaat 1200
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agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa atatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 80
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 80
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaaggtca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
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cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
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gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 81
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 81
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cgcaccggtg gaacattacc ccgccgtgca ttacgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gttacgccaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcct 300
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cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaacgtg atggaggctt cagctctcag 480

ttaaagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
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cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

<210> 82
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 82
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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
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<210> 83
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetically generated variant

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<210> 84
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

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<210> 85
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 85
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cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
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<210> 86
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 86
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ctcagagatc tcaacaatat tcctccatga 1410

<210> 87
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 87
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<210> 88
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 88
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<210> 89
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 89
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<210> 90
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 90
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<210> 91
<211> 469
<212> PRT
<213> Aspergillus terreus

<400> 91
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Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
        35   40   45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50   55   60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65   70   75   80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                85   90   95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser

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Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
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Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
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Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
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Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
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Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
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Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
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Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
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Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
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